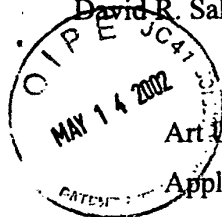


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1743
CLAIM OF PRIORITY UNDER 35 USC §119
Examining Group 1743
Patent Application
Docket No. GJE-87
Serial No. 10/081,599

David R. Saliwanchik
David R. Saliwanchik, Patent Attorney



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Art Unit : 1743
Applicants : Cornelia Anna Mundt, Marianne Brueggemann
Serial No. : 10/081,599
Filed : February 20, 2002
Conf. No. : 9658
For : Immunoglobulin Control Region

Assistant Commissioner for Patents
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CLAIM OF PRIORITY UNDER 35 USC §119

Sir:

The applicants in the above-identified patent application hereby reaffirm their claim to the right of priority granted pursuant to 35 USC §119 based upon Great Britain Application No. 0104299.3, filed February 21, 2001.

As required by the Statute, a certified copy of the Great Britain application is being submitted herewith. The applicants request that this certified copy of the foreign priority application be made of record in the subject application pursuant to MPEP 201.14(b).

Respectfully submitted,

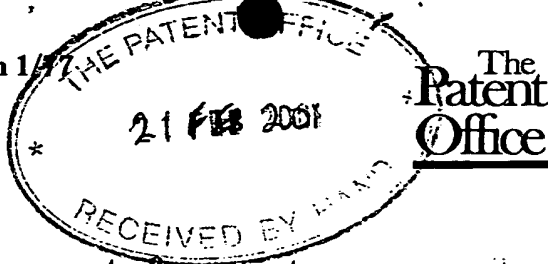
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The Babraham Institute
Babraham Hall
Babraham
Cambridge
CB2 4AT

Patents ADP number (if you know it)

07414519001

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4. Title of the invention

IMMUNOGLOBULIN CONTROL REGION

5. Name of your agent (if you have one)

Gill Jennings & Every

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IMMUNOGLOBULIN CONTROL REGION

Field of the Invention

This invention relates to a control region in human immunoglobulins, to parts thereof and to their use.

Background of the Invention

The human IgH locus contains nine functional C genes and two pseudogenes, arranged 5' C μ -C δ -C γ 3-C γ 1- ψ C ϵ -C α 1- ψ C γ -C γ 2-C γ 4-C ϵ -C α 2 3', over a 350 kb region of chromosome 14 (1). Overlapping phage and cosmid clones established the C gene organisation but attempts to obtain the entire region on overlapping clones or a single yeast artificial chromosome (YAC)⁵ have been unsuccessful (ref. 2 and our own results). PCR-based approaches identified highly repetitive regions downstream of C α 1 and C α 2 which include virtually identical 3' enhancers made up from different numbers of short motifs (3, 4). Similar repetitiveness, leading to instability, was also assumed for the estimated 40-70 kb gap between C δ and C γ 3, which could not be cloned to establish a C gene contig. Indirect results from transgenic mice lacking different regions 3' of C μ and C δ further suggested that this particular downstream region might be important for high expression and switching of IgH genes (5, 6). Analysis of recombination in the C δ -C γ 3 interval showed a lack of association between these genes, which may indicate a potential hot spot for recombination (7, 8). The potential significance of this region is further supported by the finding that a large area between C δ and C γ 3 is deleted in certain leukemias, which may be linked to a pathogenic mechanism active at an early stage of B-cell development (9).

In the mouse, the IgH locus has been completely cloned (10), and in DNA-binding assays a cluster of matrix association regions (MARs) was found in the C δ -C γ 3 intron (11). Although the region was not extensively characterized by sequencing, the presence of long interspersed repetitive elements in the vicinity of MARs may lead to the high recombination observed in this region of the IgH locus. Probes derived from bacteriophage clones covering the mouse C δ -C γ 3 region failed to identify corresponding sequences in the human locus (9). During B lymphocyte development it is generally thought that transcriptional activation of

the IgH locus is regulated using two enhancer arrays which flank the constant region cluster (12-14, reviewed in 15). These arrays, the E μ intron enhancer and the 3' enhancer downstream of C α , contain multiple sites for the binding of both tissue specific and ubiquitous trans-acting factors (13, 16). Enhancer-mediated activation appears to be controlled by the interaction of both negative and positive regulatory elements (17, 18). The E μ intron enhancer provides potential protein binding sites for several regulatory elements which are essential for lymphocyte differentiation, including E47, PU.1, Ets-1, TFE3, USF and Oct (19, 20). The 3' α enhancer shares some DNA sequence elements with the E μ enhancer but also has additional motifs for factors involved in transcriptional regulation (13, 16). Activation and sequential DNA rearrangement of the Ig loci are crucial steps in antibody expression and *cis*-acting locus elements like enhancers, which accommodate various combinations of factor binding sites, have been implicated in IgH locus recombination and transcription (17). Although important information about enhancer core functions has been obtained from mutant mouse strains, these are poorly understood processes as there appears to be no activity of either enhancer in early B-cell development when IgH heavy chain rearrangement is initiated. For example, deletion of the heavy chain intron enhancer E μ showed severe impairment of V H to D JH rearrangement whilst the earlier D to J H rearrangement was much less affected (21). In chimeric mice, in which the C α 3' enhancer was replaced by a marker gene, isotype deficiency and impairment of heavy chain class-switching was observed (18).

Summary of the Invention

The region between C δ and C γ 3, of IgH is unstable and may be a recombination hot spot; it has now been shown that 21 kb of the unstable region in the human IgH locus between C δ and C γ 3 contains a highly clustered array of a large number of transcription factor binding motifs interspersed with repeat sequences. Transfection assays revealed transcription enhancement and silencing activity at the pre B-cell stage and in transgenic mice strong enhancer function was identified in the bone marrow, the primary site of B-cell differentiation. Flow cytometry analysis of early B-cell populations showed that

this enhancer is already active at the pro/pre B-cell stage where DNA rearrangement is initiated. The region accommodating E δ - γ 3 may exert locus control function at an early developmental stage, which may be critical in normal and aberrant B-cell development.

In particular, a pBAC clone (pHulGH3' δ - γ 3) has been isolated, that established a 52 kb distance between C δ and C γ 3. Sequence analysis identified a high number of repeat elements, explaining the instability of the region, and an unusually large accumulation of transcription factor binding motifs, both for lymphocyte-specific and ubiquitous transcription activators (IKAROS, E47, Oct-1, USF, Myc/Max), and for factors which may repress transcription (DeltaEF1, Gfi-1, E4BP4, C/EBPbeta). Functional analysis in reporter gene assays revealed the importance of the C δ -C γ 3 interval in lymphocyte differentiation, and identified independent regions capable of either enhancement or silencing of reporter gene expression, and interaction with the IgH intron enhancer E μ . In transgenic mice, carrying a construct which links the β -globin reporter to the novel δ - γ 3 intron enhancer (E δ - γ 3), transgene transcription is exclusively found in bone marrow B-cells from the early stage when IgH rearrangement is initiated up to the successful completion of H and L locus recombination resulting in antibody expression. These findings suggest that the C δ -C γ 3 interval exerts regulatory control on immunoglobulin gene activation and expression during early lymphoid development.

According to a first aspect of the invention, the C δ -C γ 3 region is stable in an artificial chromosome or non-human animal. It can thus be used to produce a repertoire of human antibodies or antibody fragments in a non-human animal; the functional characteristics of the region, including effective enhancer sequences, can provide a wider and more useful repertoire than has previously been possible.

According to a second aspect of the invention, a functional enhancer and/or silencer sequence within the C δ -C γ 3 region (of the human or non-human IgH locus) can be used as such, e.g. in a heterologous construct, to enhance the

expression of a heterologous gene. For this purpose, the repeat sequences that give the C δ -C γ 3 region its instability are not needed.

Description of the Invention

Materials and methods

BAC library construction

A size-selected library was constructed from human DNA using the pBeloBACII vector (22). An MluI linker was added to the pBeloBACII vector following linearisation with SphI in the multiple cloning site. Human genomic DNA was prepared from the fibroblast cell line KB (23) and digested to completion with MluI. The fragments were size fractionated by Pulsed Field Gel Electrophoresis (PFGE) in 1% low melting temperature agarose (SeaPlaque FCM, USA) at 12V/cm in 0.5 x TBE with a 40 sec pulse for 24 h at 3.5°C. Gel slices containing DNA fragments from ~30-80 kb were excised, melted at 67°C and digested for 1 h at 40°C with 1 unit Gelase (Epicentre, USA) per 0.1 g of gel. Size selected DNA (100-200 ng) was ligated with dephosphorylated MluI restricted pBeloBACII vector (25-50 ng) using 4 units T4 ligase (NEB, Canada). Ligation mixtures were dialysed against 3 ml TE and 1mM polyamines for 4 h at room temperature using Millipore filters 30000 NMWL (Millipore, USA). Aliquots of the dialysed ligation mixture (1 μ l) were used to transform *E. coli* DH10B by electroporation at 120 V, 25 μ F, and 100 Ohms (24). Transformed cells were incubated for 90 min at 37°C in SOC medium, shaking at 250rpm, and plated on LB-agar containing 12.5 μ g/ml chloramphenicol, 50 μ g/ml X-Gal, and 25 μ g/ml IPTG. Distinguishable white and blue colonies appeared after 24h, and about 5000 white clones were isolated and analysed by colony-filter hybridization with the 0.4 kb EcoRI fragment of pM5-1-23 (25) and human C γ 3 (ref. 26 and see below). The insert size was determined by MluI digest and PFGE.

Hybridization and sequencing

For hybridization analysis, genomic DNA (10 μ g) or pBAC DNA (0.5 ng), was digested with the desired restriction enzyme and separated on 0.8 % agarose gels in TAE. DNA was transferred to nylon membranes (Hybond-N, Amersham) by alkaline transfer and the blots were hybridized with oligolabelled

probes at 65°C in Church Buffer. Hybridization probes were a 7.4 kb HindIII fragment containing human $\gamma 3$ (26) and a 0.4 kb EcoRI fragment obtained from a 3.4 kb BamHI fragment located ~20 Kb downstream of human C δ from the 3' end of the HulgH YAC, derived by plasmid rescue after digestion (clone pM5-1-23, ref. 25). The 5.9 kb BamHI fragment of pHulgH3' δ - $\gamma 3$ (see Fig. 1) was subcloned and a 0.5 kb SspI-BamHI fragment was derived therefrom for further mapping.

Sequencing was performed by the Babraham Microchemical Facility using an ABI Model 373 automated sequencer. Sequence information was obtained using vector-specific primers to analyse restriction fragments subcloned in pUC19 or overlapping fragments obtained by exonuclease III digestion of fragments (Erase-a-Base System, Promega, UK), and also by custom oligonucleotides based on initial sequence information.

Cell lines and transfection assay

The cell lines used for the reporter gene analysis were from the Institute's collection or a kind gift from collaborators and their origin is described in the American Tissue Culture Collection catalog. The human cell lines used were NALM-6 pre B-cells, DG-75 plasma cells, Jurkat T lymphoblast cells and KB fibroblasts (27 and references therein, 28, 29, 23), and the mouse cell lines were 3-1 and 18-81 pre B-cells and the plasma cell lines MPC11 (producing IgG2b) and AH (producing IgM) (30). The cell lines were maintained in RPMI (Gibco, UK) supplemented with 10% FCS and 50 μ M β -mercaptoethanol.

Transcriptional activity of fragments from the pHulg3' δ - $\gamma 3$ 5' region was analysed with a luciferase reporter assay system according to the manufacturer's protocol using a BioOrbit 1253 Luminometer (Promega, UK). The pGL3 vector ensures low background luciferase expression and this allowed the unambiguous measurement of enhancer function. The overlapping fragments from the pHulg3' δ - $\gamma 3$ 5' region (see Figs. 1 and 5) tested were: 1) 10.7 kb MluI-HindIII; 2) 7.2 kb MluI-BamHI; 3) 8.5 kb HindIII; and 4) 5.9 kb BamHI. These were inserted 5' of the SV40 promoter of the pGL3 reporter gene construct. The size of fragment 2 in the reporter gene construct was reduced by creating the necessary 5' and 3' overhang by MluI and KpnI restriction and exonuclease III treatment. As

a positive control, pGL3 control vector containing the SV40 enhancer was used. To test the interaction with other IgH enhancers, the human E μ intron enhancer (25) was added 5' of an inserted fragment. Pre B-cells, pro B-cells, Jurkat and KB fibroblasts (2.5×10^6) were transfected by electroporation using 7 μ g pGL3 containing fragment 1, 2, 3 or 4 with or without E μ and with 1 μ g pSV- β -galactosidase control plasmid as an internal standard. Electroporation conditions were 960 μ F, 200 Ohms and 270-300V. Cells were harvested after 20-22h incubation. Plasma cells ($1-3 \times 10^5$) were transfected with the above constructs by lipofection with DOTAP (Boehringer, Mannheim, Germany) according to the manufacturer's protocol. The β -galactosidase assay was performed in 100 μ l reaction buffer (0.1M Na²HPO₄/NaH₂PO₄ pH7.3; 1mM MgCl; 50 mM β -mercaptoethanol; 1.33 mg/ml o-nitrophenyl- β -D-galactopyranoside) for 30-120 min. The reaction was stopped with 150 μ l 1M Na₂CO₃, and the conversion of substrate was measured in a Titertek Multiscan MCC/340 at 410 nm.

Transgene expression analysis

The 1.3 kb E δ - γ 3 fragment (position 5885 to 7185 in pGL3) obtained by PCR was added to a 3 kb human β -globin gene subcloned in pUC12 (31) by blunt end ligation into the XbaI site in the linker. A ~4.3 kb SacI-HindIII DNA fragment containing E δ - γ 3 linked to the β -globin reporter gene was gel purified and injected into the pronuclei of fertilised (C57BL/6xCBA)F1 eggs at 1-2 pg/ml (32). Transgenic mice were obtained with high and low copy number verified by tail blot analysis with a transgene probe. RNA from different tissues was prepared as described by the manufacturer using the RNAqueous Kit (Ambion, UK) or the RNazol B method (AMS Biotechnology, Oxford, UK) for bone marrow. Cell preparations were essentially free of erythrocytes with the exception of liver cells where a low percentage remained. Hybridization probes were the β -globin transgene and a 540 bp actin gene fragment obtained by PCR (33). For the isolation of B-cell subpopulations by flow cytometry bone marrow cells were stained as described (34). Multicolor staining was carried out with the following reagents in combinations shown in Fig. 7B: PE (phycoerythrin)-conjugated anti-mouse CD25 (P3317, Sigma), PE-conjugated anti-mouse CD45R (B220) (P3567,

Sigma), biotinylated anti-mouse IgM (No. 02082D, PharMingen), PE-conjugated anti-mouse c-*kit* (CD117) (No. 09995B, PharMingen), FITC-conjugated anti-mouse CD19 (No. 09654D, PharMingen), FITC-conjugated anti-mouse IgD (No. 02214D, PharMingen) and biotinylated anti-mouse CD43 (No. 01602D, PharMingen). Binding of biotinylated antibody was developed with streptavidin quantum red (S2899, Sigma). The oligonucleotides for RT-PCR of β -globin and HPRT as a control have been described (31). RT-PCR was performed with the One-Step System (GibcoBRL) under the following conditions: 50°C for 30 min followed by 94°C for 2 min for cDNA synthesis, followed by 30 PCR cycles (15 sec 92°C, 30 sec 55°C, 30 sec 72°C) and 5 min at 72°C to complete the reaction.

Results

The distance between C δ and C γ 3 is 52 kb

Southern blot analysis suggested that the region between C δ and C γ 3 is 40-70 kb in size (1, 8). We analysed human sperm DNA and the human fibroblast cell line KB (23) by digestion with rare cutting enzymes and hybridization with probes from the 3' end of the human IgH YAC and from human C γ 3 (see Fig. 1). Southern blots of MluI digests showed a possible region of ~50 kb capable of spanning the gap between C δ -C γ 3 (data not shown). A size selected bacterial artificial chromosome (BAC) library was constructed and hybridized with the 0.4 kb EcoRI fragment of pM5-1-23, from the 3' end of the IgH YAC (25), and human C γ 3 (26). Of eight clones, pHuIgH3' δ - γ 3, hybridized with both of these probes and MluI restriction digestion followed by Pulsed Field Gel Electrophoresis (PFGE) identified a 48 kb insert. Comparison of the restriction patterns of pHuIgH3' δ - γ 3 with the HuIgH YAC (5) and coslg6 (35) revealed substantial homologies at the 5' and 3' ends respectively, which suggested that pHuIgH3' δ - γ 3 spanned the gap between the C δ and C γ 3 constant region genes (Fig. 1A). The 5' MluI cloning site of pHuIgH3' δ - γ 3 lies ~4 kb 3' of the δ membrane exon 2, a region not yet characterized by sequence analysis, whilst the 3' MluI cloning site is located in the hinge region of C γ 3 (36). Alignment of restriction maps of pHuIgH3' δ - γ 3 with the HuIgH YAC and coslg6 identified a novel 11 kb region.

To verify that this novel region is in the correct genomic configuration, different digests of human DNA and pHulGH3' δ - γ 3 DNA were analysed in Southern blots using different hybridization probes. An example (Fig. 1B) shows that hybridization with the 0.5 kb SspI-BamHI fragment from pHulGH3' δ - γ 3 identified a 5.9 kb BamHI fragment and a 8.5 kb HindIII fragment both of which are present in human genomic DNA and pHulGH3' δ - γ 3. The C δ proximal BamHI site and the C γ 3 proximal HindIII site of the hybridization fragments are also present on the IgH YAC and cos Ig6, respectively. These results confirm that the cloned region on pHulGH3' δ - γ 3 completes the C δ -C γ 3 sequence gap and establishes the distance between C δ m2 and C γ 3 as 52 kb.

The C δ -C γ 3 interval region is highly repetitive

The nucleotide sequence of the C δ proximal 5' region of pHulGH3' δ - γ 3 (EMBL no. to be added), indicated in Fig. 1A by the hatched line, was determined by subcloning of overlapping fragments, exonuclease III digestion and primer walking. Self-alignment of this 21 kb region (Fig. 2A) identified many regions of similarity as Alu motifs (37), with a pronounced cluster at the 3' end (Fig. 2B) that incorporated several residual fragments of Alu motifs as well as complete motifs, in various orientations. In addition, we found transposon-like elements (LINE, LTR etc.) in abundance and of different complexity (38-40); three 40 bp MstII-like repeats were arranged in a tandem configuration, which may highlight transposon activity, and a 76 bp region comprising 23 (CT) repeats was followed immediately by 15 (AT) repeats. The CT and AT repeats encode the amino acids pairs Leu/Ser and Ile/Tyr independently of the reading frame. The presence of this large number of repetitive elements may be the reason for the instability of the locus observed during cloning efforts.

A cluster of transcription factor recognition motifs

Potential binding factor recognition sites of regulatory proteins were identified by comparison of the pHulGH3' δ - γ 3 sequence with the TRANSFAC transcription-factor database using Matinspector (41, 42). As shown in Fig. 3, many binding motifs were represented very frequently despite the high score used for the database search, which was 1.0 for core similarity and 0.90 or

greater for matrix similarity. The transcription factors identified can operate either to enhance or suppress immunoglobulin transcription, and many are also present in the E μ and 3' α enhancer regions (reviewed in ref. 43, 44). Binding sites were found for the activating proteins Ikaros, E47, Oct1, USF and Myc/Max (45-51). The Ikaros gene products belong to the group of zinc finger DNA binding proteins (52) and have a complex role in the early stages of lymphocyte development with establishing the maintenance and differentiation of multipotent progenitors (53). In the group of repressor proteins, binding sites for DeltaEF1, Gfi-1, E4BP4 and C/EBP β were identified (54-57). The potential binding-site of the nuclear zinc finger protein Gfi-1 (growth factor independence 1) has been identified in a large number of eukaryotic promoter-enhancers (58, 59).

No similar large accumulation of different binding protein recognition sites was evident when other regions of the immunoglobulin H and L chain introns, including known enhancer regions, were examined. The presence of such an extensive and varied cluster of transcription factor binding motifs may suggest that the region between C δ and C γ 3 exerts previously unrecognised Ig locus control function.

Pre B-cell specific enhancer activity downstream of C δ

To determine any functional significance of the C δ -C γ 3 interval in development and whether the region contained new cis-acting regulatory sequences we analysed transcriptional promoter activity of subcloned fragments from pHuIgH3' δ - γ 3 using the luciferase reporter gene assay. The analysis identified a 7.2 kb MluI-BamHI fragment from the 5' C δ proximal region which showed good enhancer activity in human and mouse pre B-cells (NALM-6 and 3-1) when placed 5' of the luciferase reporter, but did not promote luciferase activity in human or mouse plasma cells (Figs. 4 and 5). As other fragments did not exhibit B-cell specific enhancer activity we wondered if the failure to demonstrate enhancer activity in Ig2b producing MPC11, in which the C δ -C γ 3 intron regions are deleted, was a consequence of the IgH locus having undergone isotype switching in this cell line. This was not the case as IgM producing AH myeloma cells produced very similar results for all fragments (data not shown). In addition,

the orientation of the subcloned fragments did not alter their functional activity and enhancer function of the MluI-BamHI fragment in pre B-cells was maintained in both transcriptional orientations.

To determine the precise location of this novel IgH δ - γ 3 intron enhancer we dissected the MluI-BamHI fragment by MluI and exonuclease digestion which removed the 5' region and resulted in various smaller size fragments (Fig. 4A). In murine pre B-cells, enhancer activity of the whole region (position 1-7185) exceeds that of the E μ enhancer but the most dramatic increase, twice the activity of E μ , was obtained with a 1.3 kb fragment from position 5885 to 7185 (Fig. 4B). In comparison to mouse cells human NALM-6 pre B-cells showed marked reductions in transcriptional activation. This may simply be a reflection of reduced transfection efficiencies of the human cells but could also indicate concerted interaction of several functional motifs which are recognized differently in mouse and human pre B-cells. However, the strongest transcriptional activation in both human and mouse pre B-cells was obtained by the fragment from position 5885-7185. Comparable enhancer activities, dependent on the developmental stage of the cell rather than its species of origin, agrees with what has been found for other human Ig enhancers analysed *in vitro* and in transgenic mice (31, 60, 61). No enhancer activity was obtained at the later developmental stage of the plasma cell (Fig. 4C). In addition, neither fibroblasts (as control cells) nor T lymphocytes showed any enhancer activity (data not shown). These results from reporter gene transfection assays define a novel region which we named E δ - γ 3 with strong cis-acting enhancer function operative at the pre B-cell stage.

A transcription silencer is located adjacent to the enhancer

The proximity of E μ and E δ - γ 3 led us to speculate about possible enhancer co-operation during B-cell development. For this we added the human E μ intron enhancer to 4 separate but overlapping fragments of the 21 kb sequenced 5' region of pHuIgH3' δ - γ 3 and measured transcriptional activity in luciferase reporter assays (Fig. 5). It is interesting to note that except in one combination (E μ + fragment 1) enhancer activity remained by and large as identified in single enhancer/fragment constructs analysed in B-cell subsets. This

suggests separate functions of $E\mu$ and $E\delta\text{-}\gamma 3$ and that their enhancer activities are not simply additive. Enhancer activity was maintained when $E\mu$ was combined with fragments 2, 3 and 4, whilst the combination of $E\mu$ with fragment 1 completely abolished enhancer activity in pre B-cells and significantly reduced enhancer activity in plasma cells (Fig. 5B). This suggests that fragment 1 contains a B-cell specific transcription silencer which is likely to be located at the 3' end of fragment 1. Fragment 4 shares a corresponding region and this may explain why transcription levels are somewhat reduced in pre B-cells when coupled to $E\mu$. Furthermore, fragment 1 contains the silencer in close proximity to the $E\delta\text{-}\gamma 3$ enhancer identified on fragment 2. Thus, the lack of enhancer activity of fragment 1 can be explained by the presence of a strong B-cell specific silencer in this region. It emerged that further dissection of the fragments was ineffective, as $E\delta\text{-}\gamma 3$ enhancer and silencer activity was reduced or abolished, and suggests that recognition motif combinations are essential. The results show that the 5'C δ -C $\gamma 3$ region accommodates a previously unidentified B-cell specific enhancer-silencer array which may interact with $E\mu$ to control Ig expression during developmental processes. However, the many varied sequence recognition motifs in the C δ -C $\gamma 3$ interval, together with the coordinated enhancer interaction identified, indicate a more complex activity with perhaps other transcription modifiers.

In transgenic mice $E\delta\text{-}\gamma 3$ is active in the developing B-cell

To determine *in vivo* specificity of the novel enhancer we constructed a transgene composed of $E\delta\text{-}\gamma 3$ linked to human β -globin as a reporter gene (Fig. 6A). A high and a low copy number transgenic mouse line with head to tail integration of the transgene was identified by Southern blot (Fig. 6B) and RNA was prepared from different tissues for Northern analysis and RT-PCR. For the assays actin or HPRT transcripts were used as internal controls. In Northern hybridization we were surprised to find β -globin expression in the bone marrow and not in other B-lineage tissue (Fig. 6C) which suggests an essential role of $E\delta\text{-}\gamma 3$ in B-cell development. We then used RT-PCR as a more sensitive method to analyse various B-lineage, T-lineage and non-lymphoid tissues. The result was

the same, the E δ - γ 3 driven transgene is silent in all non-lymphoid tissue as well as in the T-cell compartment, and extensive β -globin specific transcription is only found in bone marrow RNA. These results and the *in vitro* reporter gene assays suggest differentiation stage specific activity of E δ - γ 3 from pro B-cell development (initiation of DNA rearrangement) to mature B-cell (surface IgM) prior to migration from the bone marrow.

To identify differentiation stage specific cell populations in which E δ - γ 3 is active we used flow cytometry and RT-PCR (Fig. 7). The progressive stages in B-cell development are well characterized by cell surface markers and DNA configuration (62). We isolated several distinct cell populations from the bone marrow identified by staining with labelled antibodies specific for the B-cell markers B220 or CD19 in combination with specific antibodies for *c-kit* and CD43 (pro B and pre B-I stage), CD25 (pre B-II stage) and IgM/IgD (immature to mature B-cell) (Fig. 7B). RT-PCR identified β -globin activity in B220⁺ or CD19⁺ B-cells from bone marrow up to the immature IgM⁺IgD⁻ population which has completed the DNA rearrangement process. Transgene activity may be initiated at the early pro B-cell stage in *c-kit*⁺ B220⁻ cells where a faint β -globin specific PCR band (relative to the HPRT signal obtained in the same reaction) was found. As the number of *c-kit*⁺CD19⁻ cells was very low this result may have been obtained from a small cross-contamination of the more abundant CD19⁺ cell population. However, at the stage when DNA rearrangement, D to J_H joining, is initiated in *c-kit*⁺CD19⁺ and CD43⁺B220⁺ B-cells (63) the E δ - γ 3 enhancer is active. H chain and largely L chain rearrangement is finalised at the immature B-cell stage and cells expressing surface IgM show that E δ - γ 3 driven β -globin expression is extinguished at this maturation stage. This concludes that the E δ - γ 3 enhancer is active at the earliest DNA rearrangement event and silent when the rearrangement process (V-D-J for the H chain and V-J for a L chain) has been successfully completed.

Discussion

Instability of the C δ -C γ 3 interval

Use of the BAC cloning system, capable of maintaining highly repetitive large insert DNA (22, 64), enabled us to establish the distance between C δ m2 and C γ 3 as 52 kb. Southern analysis and alignment of pHuIgH3' δ - γ 3 with the 3' end of the HuIgH YAC (5) and the 5' end of coslg6 (35) confirmed the overlap and identified a novel region of 11 kb. The failure of previous attempts to clone the C δ -C γ 3 contig in cosmids or YACs can now be fully explained by the extensive repetitiveness of the intronic sequence. Such repetitive regions are prone to deletion through homologous recombination when cloned in yeast (65). It is estimated that Alu-like repeat sequences are represented on average every 4 kb throughout the genome (66, 67). In the interval from C δ m2 to C γ 3, 11 Alu-like repeats were identified in a 15 kb region. In contrast, the number of Alu motifs identified in the 950 kb region containing the variable genes of the human IgH locus was much less than expected by random distribution (68). The presence of Alu repeat elements immediately adjacent to proto-oncogene translocations has led to the suggestion that frequent Alu motifs may predispose a region as a hot spot for recombination (69, 70). Indeed, the MstII-like sequences, identified in tandem in the C δ -C γ 3 interval, align with the consensus sequence of transposon-like elements in the human genome (39, 40). The instability of the region is further supported by linkage data, which indicate a lack of association between C δ and C γ 3 (7) and that certain leukemias have deletion boundaries in the C δ -C γ 3 region (9). Thus, translocations near the enhancer-silencer array in the C δ -C γ 3 interval may result in transcriptional alterations of the rearranged genes or loci leading to a malignant phenotype of the cell subset where enhancer activity can be identified. Interestingly, chromosomal translocations in Burkitt's lymphoma where *c-myc* expression is deregulated by linkage to a known enhancer may represent tumors of a developmental stage in which the enhancer is active.

A Factor binding site cluster

The frequency of potential transcription factor binding sites in the 21 kb of the C δ -C γ 3 interval region sequenced was unexpected. Using the default scores for the analysis, 0.75 for core similarity and 0.85 for matrix similarity (41) identified too many motifs to be useful. Our analysis used scores for the core similarity of 1 and matrix similarity of 0.90. This higher score allowed the unambiguous identification of multiple motifs for 9 transcription factor binding sites, five of which are recognised by proteins that have shown to increase transcription in lymphocytes (Ikaro, E47, Oct-1, USF and Myc/Max) and four motifs shown to be recognised by transcription silencer or repressor proteins (DeltaEF1, Gfi-1, E4BP4 and C/EBPbeta). It has been shown that the repressor proteins Delta-EF1 and Gfi-1 interact with elements of the E μ enhancer (59, 58). However, it is not obvious how the lymphocyte-specific enhancer and repressor activity identified by functional analysis of C δ - γ 3 interval fragments relates to this accumulation of potential transcription factor binding motifs. Core sequence motifs for factor binding sites found in E μ also occur frequently in this novel enhancer region and, indeed, in the whole 21 kb region analysed (see Fig. 3). That all 9 binding sites appear frequently throughout the E δ - γ 3 interval makes it impossible to predict the activity of a particular region solely based on the nucleotide sequence. Furthermore, besides short sequence motifs no homology to draw conclusions about functional similarity was found between the MluI-HindIII fragment accommodating E δ - γ 3 and the E μ or 3' α enhancers (71-74). Similarly, the region responsible for the transcription silencer activity could not be deduced from sequence comparison. However, because of the significance of the functional activity identified in the C δ - γ 3 interval it is unlikely that the motifs in this cluster are randomly distributed. In addition, recognition sequences essential for suppressing the function of the mouse 3' enhancer have been reported (30), but were not evident in the sequenced region. Sequence comparison of human E δ - γ 3 with the available mouse δ - γ 3 interval sequence did not allow identification of an equivalent mouse enhancer; however, a reason for this could be the apparent sequence gaps.

An essential role of the C δ -C γ 3 interval in early lymphocyte development

The location of the C δ -C γ 3 interval means that it will be deleted after switching from C μ to other isotypes. This implies that the regulatory activity of this region must be important during early developmental steps, which is supported by our finding that E δ - γ 3 enhancer control is operative at the pro/pre B-cell stage (see Fig. 7). Reporter gene assays suggest that the C δ -C γ 3 interval region provides strong B-cell specific enhancer and repressor function. The strength of E δ - γ 3, position 5885-7185, can be 2-fold greater than E μ enhancer activity in pre B-cells, but unlike E μ and E α 3' the δ - γ 3 interval enhancer does not exhibit any activity in mature B-cells. Interestingly, E δ - γ 3 activity is solely B-cell specific unlike that of E μ which shows some activity in T-cells at the developmental timing of rearrangement (75). At developmental stages where neither the E μ nor the E3' α enhancer was particularly active by itself, enhancer combinations identified synergistic transcriptional activity (76). A different picture emerged when C δ - γ 3 interval fragments in combination with E μ were transfected (Fig. 5). Here individual enhancer function remained cell type specific rather than synergistically increased; in E δ - γ 3+E μ constructs the activity equalled that of E δ - γ 3 in pre B-cells whilst E μ levels were obtained in plasma cells. The identified silencer extinguished both enhancers at the pre B-cell stage which suggests a complex, yet to be explored, regulatory function of elements in the E δ - γ 3 interval which appear to coordinate stage specific H chain activation. When linked to a β -globin gene (that does not contain any cell-type specific intragenic regulatory elements active in hematopoietic cells) and assayed in transgenic mice, E δ - γ 3 is a B-cell specific transcription enhancer element active during B-cell development in the bone marrow. This pattern of activity complements the transcriptional activities of E μ and E3' α , contributory to V to DJ joining, switching and H chain expression (18, 21, 77, 78), and may suggest a role of E δ - γ 3 in heavy chain activation and/or initiation of DNA rearrangement. A view that the presence of several enhancers in the Ig loci simply reflects redundancy cannot be supported with these results which put the functional activity of the IgH enhancers in a

possible order. Starting with the earliest, E δ - γ 3 may be important for H chain activation with initiation of DNA recombination; E μ may then complete the joining process to allow H chain expression; E μ may also be involved in facilitating isotype switching; E α 3' may complete the switching process, which also deletes E μ and E δ - γ 3, and may have a role in influencing expression.

The high frequency of transcription factor binding sites and the functional activity of the C δ -C γ 3 intron, which includes an enhancer-silencer array, is reminiscent of the locus control regions (LCRs) described for the globin locus (79, 80). It is characteristic of LCRs that they are essential for the correct activation of a locus to ensure physiological expression levels are obtained. In transgenic mice carrying part of the human IgH locus, high level expression of the transgenes independent of copy number and integration site was not achieved (5). This suggests that neither the E μ nor the 3' enhancer region are sufficient in themselves to ensure the full activity of a single copy translocus. In transgenic mice it will be interesting to see if a translocus that includes a complete C δ -C γ 3 interval allows correct chromatin opening and gene activation. Identification of an equivalent region in the mouse and its removal by a knock-out approach may shed further light on IgH locus activation and the DNA recombination processes which are still poorly understood.

Construction and expression analysis of the human IgH YAC has been described in Nicholson *et al*, J. Immunol., 163, 6898-6906, 1999, and techniques to manipulate YACs by extension have been described by Popov *et al*, Gene, 177, 195-201, 1996.

The extension of the hulgH YAC by adding a (γ) 3 constant (C) region allows to study isotype switching. We used two strategies to obtain a human IgHG3 YAC: 1) addition to the γ 3 region on a cosmid to the hulgH YAC and 2) cloning of the authentic ~50 kb region between C δ and C γ 3 in pBAC and elongating the hulgHG3 cosmid YAC by addition of this region. This produced an ~300 kb human IgH region containing the authentic germ line region from VH2-5 to downstream of C γ 3.

In detail, the experiments were done in the following way:

- 1) hulgH YAC-containing yeast cells were co-transfected with BssHII linearised coslg6 (the C γ 3 containing cosmid produced by Flanagan and Rabbitts, *Nature*, 300, 709-713, 1983) and a non-centromeric YAC arm replacement containing ADE2 as selectable marker (Markie *et al*, *Somat. Cell. Mol. Genet.*, 19, 161-169, 199). This allowed tandem integration and selection of modified YACs. IgG3 YACs were initially identified by PCR and further analysed by normal gel electrophoresis and pulsed field gel electrophoresis on Southern blots. IgH yeast clones containing the complete γ 3 cosmid region in correct transcriptional orientation, integrated in the predicted way, were used in protoplast fusion of yeast and ES cells. The resulting hulgHG3 ES cell clones were further analysed for gene content. Four different hulgHG3 clones modified as shown in Fig. 8 were used to produce chimeric mice and also resulted in germ line transmission mice. Expression of human IgG3 was found in all four founders but the levels identified in ELISA assays were relatively low (ng/ml). Breeding into the μ MT background (a mouse strain with silenced mouse heavy chain locus, Kitamura *et al*, *Nature*, 350, 423-426, 1991) may give more efficient human IgG3 expression.
- 2) The human IgHG3 YAC with the integrated cosmid DNA contains a deletion of vital regulatory sequences identified on a pBAC clone which covers the rather unstable region between C δ and C γ 3 (see above). In order to produce a YAC with the authentic region from the VH cluster downstream of the γ constant region genes we co-transformed the cosmid containing γ 3 YAC with the MluI linearised pBAC and the HIS5 gene as a selectable marker (Nishiwaki *et al*, *Mol. Gen. Genet.*, 208, 159-167, 1987). The HIS5 gene was subcloned into URA3, a gene present on the non-centromeric YAC arm. Both genes/regions, pBAC and HIS3 in URA3, allow homologous integration into the YAC and correct integration was identified by PCR and Southern blot (Fig. 9). YAC-ES cell protoplast fusion was carried out and the resulting clones were analysed by Southern blot and PCR. Two clones were used to obtain chimeric mice which are currently breeding to obtain germ line transmission.

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Abbreviations used herein: BAC, bacterial artificial chromosome; LCR, locus control region; MAR, matrix association region; PFGE, pulsed field gel electrophoresis; YAC, yeast artificial chromosome.

Figure legends

FIGURE 1. Location of the pBAC clone pHu3' δ - γ 3 spanning the gap in the C δ -C γ 3 interval region of the human IgH locus. A, Restriction analysis shows that the 48 kb MluI fragment present in pHuIgH3' δ - γ 3 (bottom) aligns with the 3' end of the HuIgH YAC (middle, left) and the 5' end of Cosmid Ig6 (middle, right), with the gap indicating the previously uncloned region of the C δ -C γ 3 interval (top). The hatched region in pHuIgH3' δ - γ 3 was sequenced and fragments were analysed in reporter gene assays. M, MluI; X, XhoI; B, BamHI; H, HindIII; E, EcoRI. (▼) 400 bp EcoRI fragment of plasmid pM5-1-23; (●) γ 3 gene probe; (◆) 500 bp SspI-BamHI fragment from pHuIgH3' δ - γ 3. B, Hybridization of BamHI or HindIII digested human sperm DNA and pHuIgH3' δ - γ 3 DNA with the 500 bp SspI-BamHI fragment derived from pHuIgH3' δ - γ 3 confirms that the isolated fragment linking the C δ -C γ 3 gap is in the correct germline configuration.

FIGURE 2. Analysis of nucleotide sequence of pHuIgH3' δ - γ 3. A, Dot Plot of self-alignment of the 5' 21 kb of the cloned region between C δ and C γ 3 starting at the 5' MluI site (see Fig. 1 for restriction sites) using the MacVector 6.01 program

(Oxford Molecular, Oxford, UK). The location of the eleven Alu-repeat-like sequences are indicated as boxes below the matrix with arrows indicating the orientation of the repeat. Three other regions of repetitive sequence are indicated by vertical arrows. Region 1 comprises three consecutive MstII-like elements. Region 2 comprises a region of 21 repeats of "CT" followed by 15 repeats of "AT". Region 3 comprises several complete and fragmented Alu motifs, as shown in B. B, Detail of the Alu motifs and fragments in region 3. The orientation of the Alu motif, indicated by a shaded box followed by an unshaded box, is indicated by arrows. The combination of a shaded box followed by an unshaded box forms an Alu-repeat-like element (large filled arrows). Separate unshaded boxes represent incomplete Alu motifs in the orientation indicated.

FIGURE 3. Location of transcription factor recognition motifs. The sequence of the 5' 20696 bp of the cloned fragment was compared to the TRANSFAC database using MatInspector, with a score of 1.0 for core similarity and ≥ 0.9 for matrix similarity (41). Restriction sites are indicated for alignment (see Fig. 1); MluI (M), BamHI (B) and HindIII (H). The potential transcription factor binding sites are indicated by open boxes. Factors which may enhance transcription in lymphocytes include Ikaros (81, 82, 52), E47 (83), Oct-1 (84, 85), USF (45), and Myc/Max (51). Factors which may suppress transcription include DeltaEF1 (56), Gfi-1 (58), E4BP4 (54, 86, 87), and C/EBPbeta (88).

FIGURE 4. Transcription enhancer activity of fragments obtained from the MluI-BamHI region of pHuGH3 δ - γ 3. A, Location of the subcloned fragments (from position 4510, 5555, 5885, 6461 and 6884 down to position 7185) with the shaded region marking the MluI-BamHI fragment (1-B), position 1 to 7185. The subcloned fragments were analysed using luciferase reporter gene assays to detect enhancer activity in B, murine pre B-cells (3-1, black bars) and human pre B-cells (NALM-6, striped bars) and C, murine plasma cells (MPC11, shaded bars) and human plasma cells (DG-75, lined bars). Experiments using murine 18-81 pre B-cells gave similarly positive results. No enhancer dependent activity was found for AH murine plasma cells, the human T lymphoblast cell line Jurkat or human KB fibroblasts (data not shown). Bars indicate luciferase activity for the

different fragments: 4510-B, 5555-B, 5885-B, 6461-B and 6884-B which are different length 3' clones obtained by exonuclease digest of the 1-B fragment subcloned in pGL3 (see Fig. 5). The luciferase activities were normalised to the β -galactosidase activity of the co-transfected plasmid and expressed as fold-increase. Values are averages of four to six independent experiments with at least two different DNA preparations. The range of standard deviation is shown in Fig. 5. Values were also determined for pGL3 vector alone, for pGL3 containing the SV40 promoter, and for pGL3 containing human E μ .

FIGURE 5. Transcriptional activity of various pHulg3' δ - γ 3 fragments in combination with E μ . *A*, Schematic diagram of the luciferase reporter gene construct with location of the insert fragments and position of E μ . *B*, pHulgH3' δ - γ 3 map and location of the subcloned fragments (left). Transcriptional activity, with standard error indicated, of fragments 1 (MluI-HindIII), 2 (MluI-BamHI), 3 (HindIII) and 4 (BamHI) with (shaded box) and without E μ (white box) was determined in pre B-cells and plasma cells. Assay details are described in Fig. 4 and in Materials and Methods.

FIGURE 6. Transgene construct, transgenic mouse identification and transcription analysis. *A*, Structure of the transgene linking E δ - γ 3 (position 5885-7185, see Fig. 4) and a human β -globin reporter gene (31). *B*, Southern blot hybridization of NcoI digested tail DNA from transgenic founders carrying the E δ - γ 3- β -globin transgene. The internal NcoI fragment is ~1.2 kb and head to tail integration produces a ~3.2 kb band. The copy number (high copy number founder 3823, low copy number founder 3832) is reflected by the signal intensity. *C*, Northern blot hybridization of different tissue samples as indicated (BM, bone marrow; PPs, Peyer's patches) with the β -globin transgene (β G) and an actin probe (33) as standard. A transgene specific hybridization signal for β -globin was only found for bone marrow RNA. Human blood and normal mouse spleen RNA served as a control.

FIGURE 7. Molecular characterization of B-cell subpopulations at various stages of development. *A*, Schematic presentation of B-cell development from

stem cell to antibody secreting plasma cell. DNA rearrangement steps for the heavy chain (D to J_H and V_H to DJ_H) and the light (L) chain (V_L to J_L) leading to surface expression and secretion of Ig are indicated. L chain rearrangement is preceded by expression of surrogate L chain (ΨLC) and gp130/gp50. Expression of the differentiation stage specific surface markers, B220, CD19, CD25, *c-kit* and CD43, is indicated by arrow bars. B, Flow cytometric isolation of *c-kit*⁺ CD19⁻ [1], *c-kit*⁺ CD19⁺ [2], CD43⁺ B220⁻ [3], CD43⁺ B220⁺ [4], CD25⁺ CD19⁺ [5] and IgM⁺ IgD⁻ [6] bone marrow B-cell populations. C, RT-PCR amplification of sorted cell populations 1-6, bone marrow (bm) and human red cells (HRC) with a combination of β-globin (βG) and HPRT primers as indicated. A strong β-globin PCR product was found in B220⁺ cells from the pro/pre B-cell type up to the immature B-cell. High copy number mice were used for the analysis shown but low copy number mice gave essentially the same result.

CLAIMS

1. An artificial chromosome including a region, between C δ and C γ 3, of the human IgH locus, or a functional part thereof.
2. A chromosome according to claim 1, which is a bacterial, yeast, eukaryotic or mammalian chromosome.
3. A non-human animal capable of producing human antibodies, and which has been transformed to include a region, between C δ and C γ 3, of the human IgH locus, or a functional part thereof.
4. An animal according to claim 3, which is a rodent, sheep, horse, pig, goat, rabbit, chicken or cow.
5. A repertoire of human antibodies, obtainable from an animal according to claim 3.
6. A repertoire of heavy chains, obtainable from an animal according to claim 3.
7. A polynucleotide comprising at least a functional enhancer or other expression modifier present in the region, between C δ and C γ 3, of the IgH locus, and a heterologous gene under the control of the modifier.
8. A polynucleotide according to claim 6, wherein the modifier comprises E δ - γ 3.



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Andrew Gersey

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1. *Chlorophyll a* and *Chlorophyll b* were determined by the method of Arar and Collins (1971). The concentration of chlorophylls was expressed as $\mu\text{g mL}^{-1}$ of the sample.

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1. *Journal of the American Medical Association*, 1997; 277: 103-107.

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the 1990s, the number of people in the world who are under 15 years of age is expected to increase from 1.1 billion to 1.5 billion. The number of people aged 65 and over is expected to increase from 250 million to 450 million. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion.

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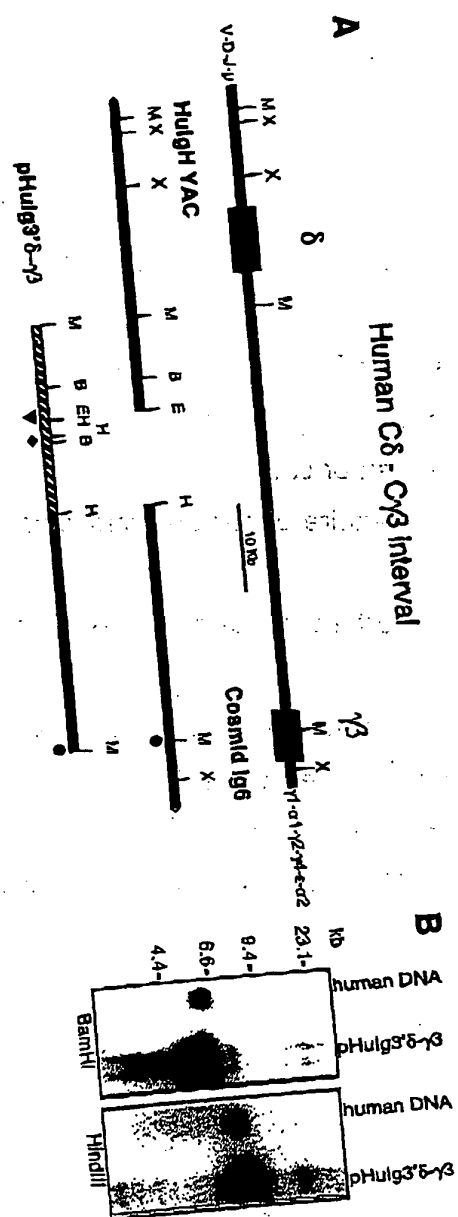


FIG. 1

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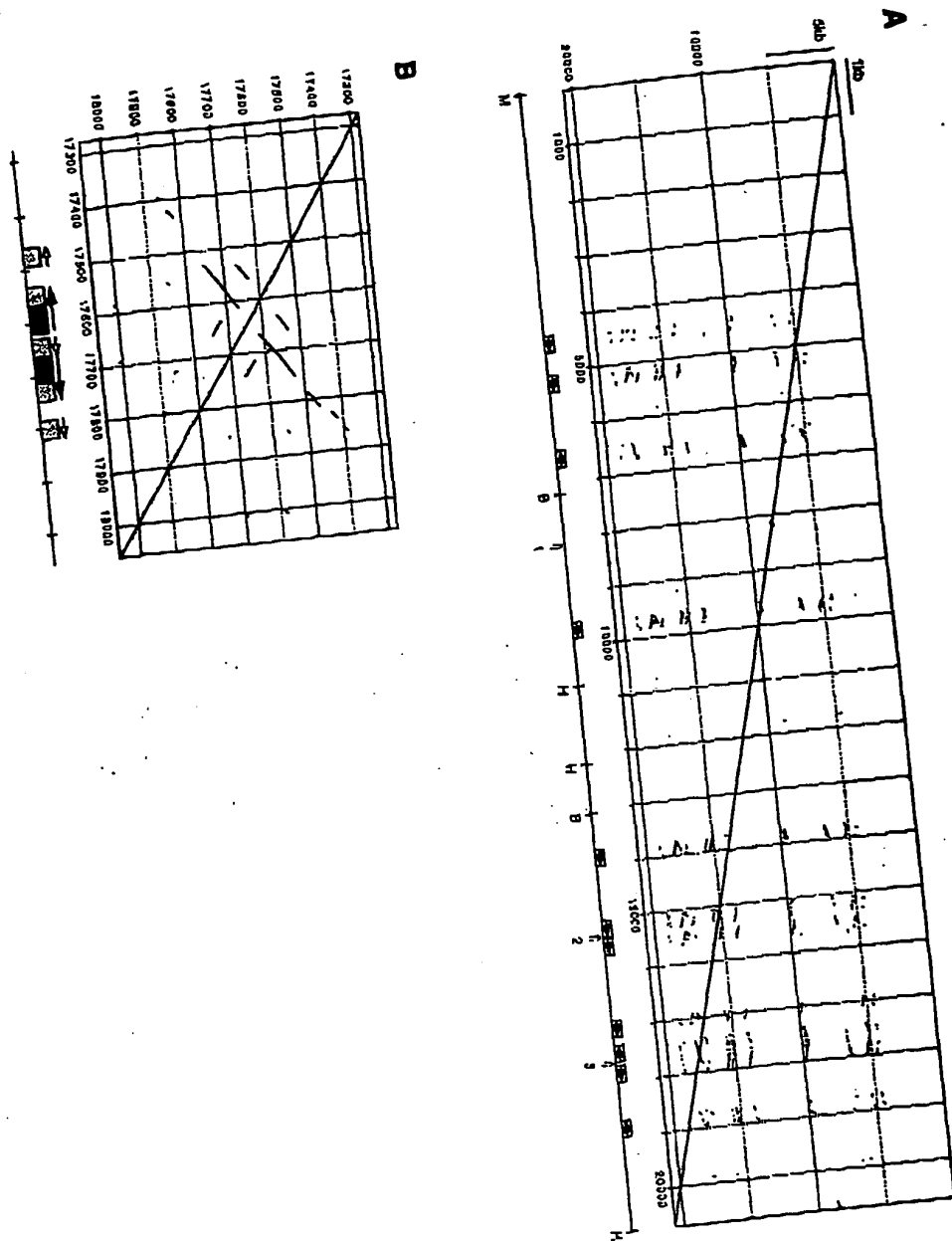


FIG. 2

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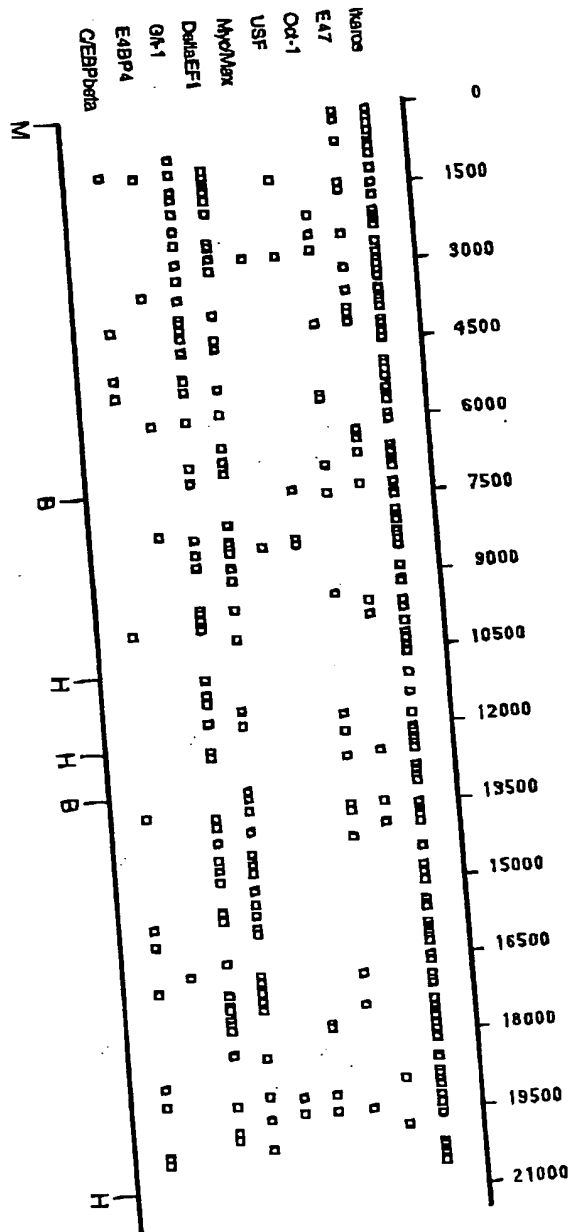


FIG. 3

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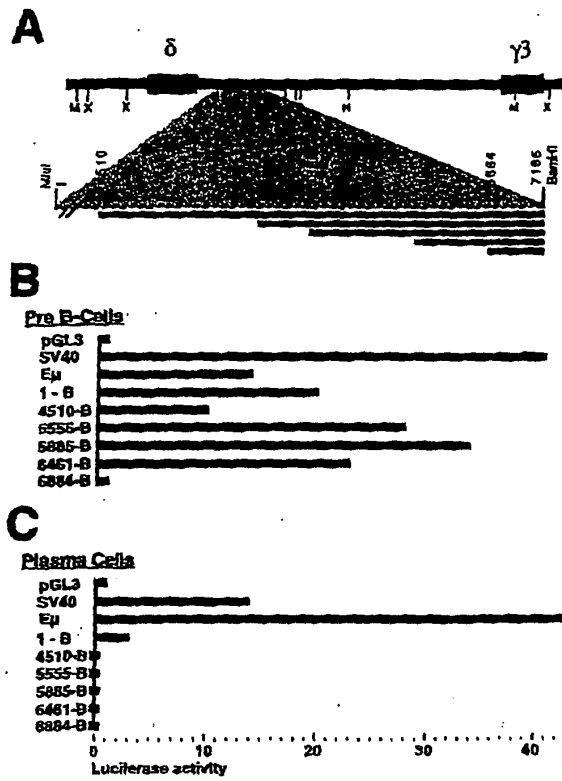


FIG. 4

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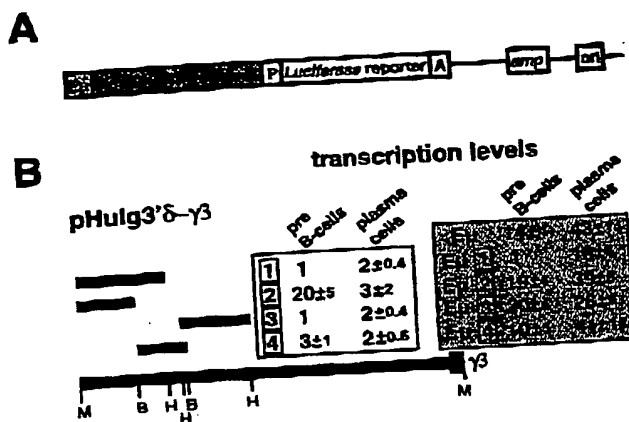


FIG. 5

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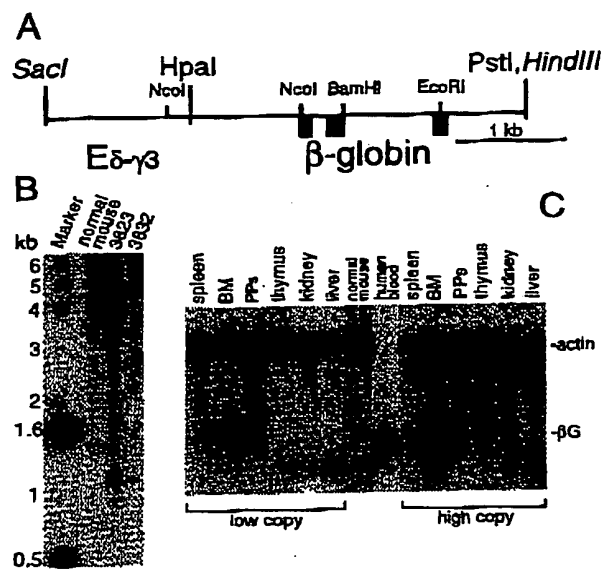
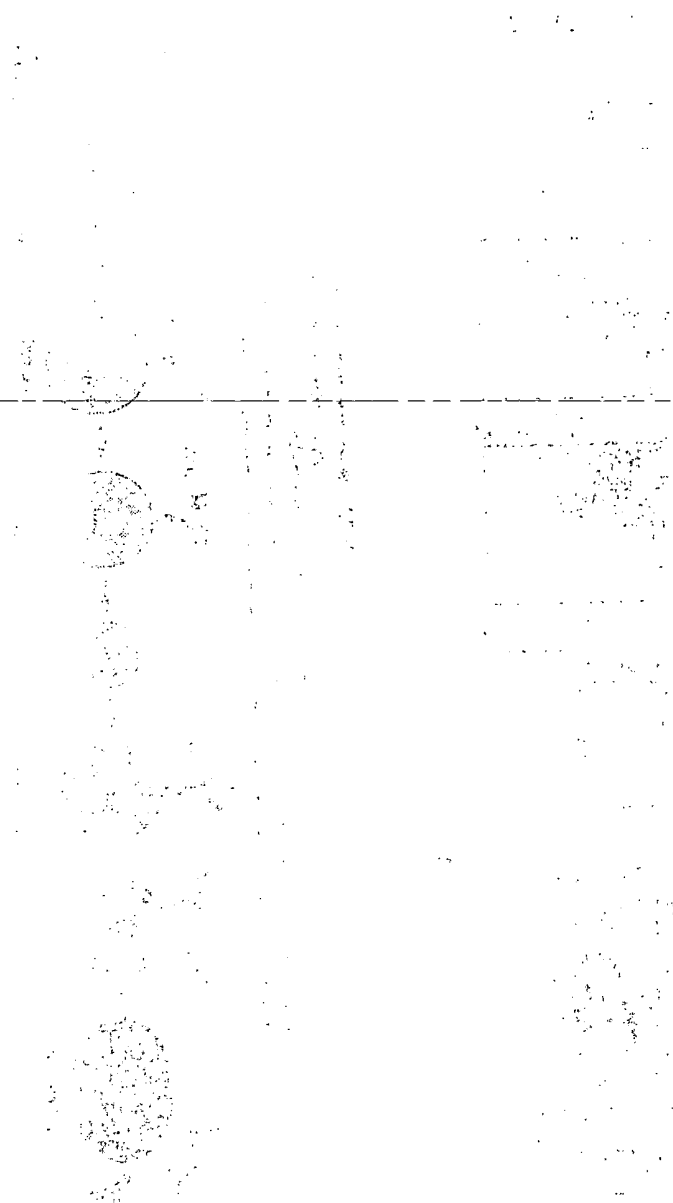


FIG. 6

Fig. 6



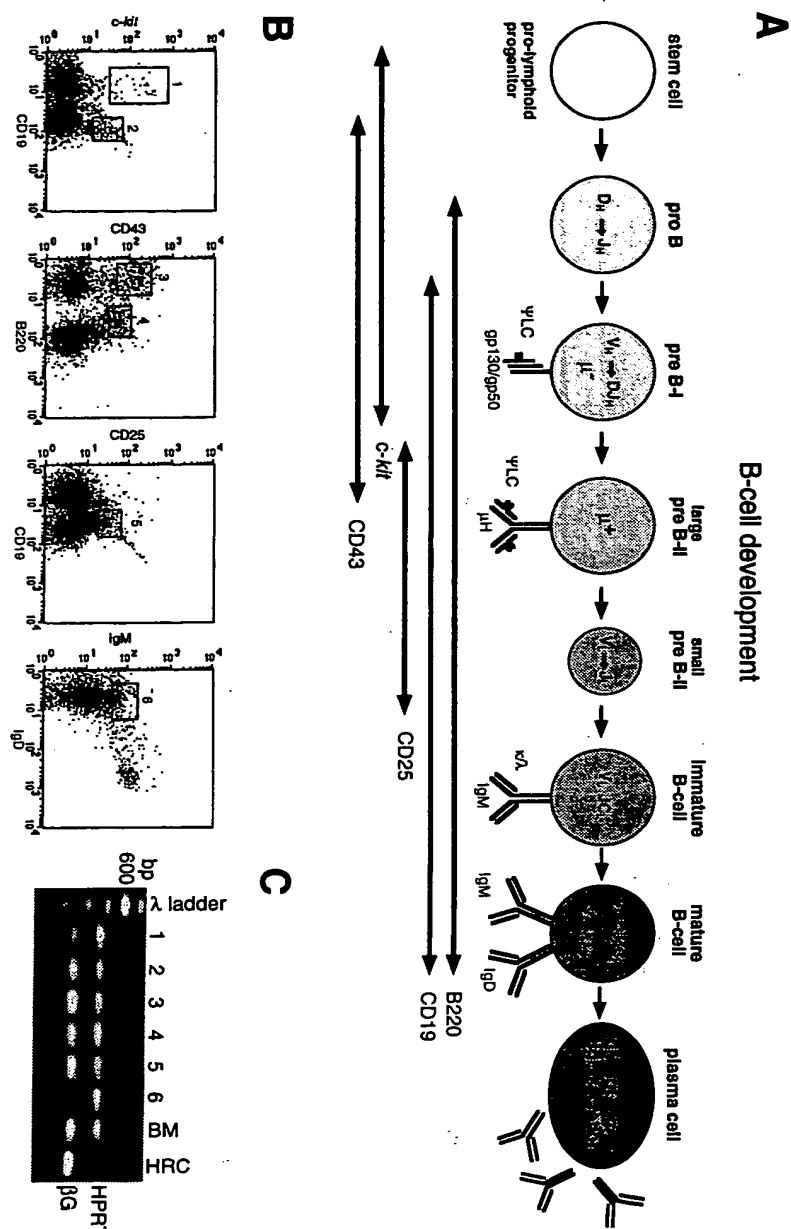


FIG. 7

Human IGHG3 Translocus



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Human IgHC3 Translocus



